

OMICS-CATALOG: a FAIR toolkit for fast visualization of omics data and metadata

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OBJECTIVE

IFREMER research teams collect numerous omics data sets that should be analyzed as quickly as possible. Therefore, the challenge for a Bioinformatics Core Platform consists in providing tools to inventory, explore and interpret those data as quickly as possible, too.

FAIR TOOLKIT

To tackle this challenge, we have developed Omics-catalog, a simple FAIR toolkit, for fast visualization of omics data and metadata. The Omics-catalog also offers an easy way to share omics information at various levels (private, restricted or public access).

nextflow PIPELINE

Omics-catalog is based on a Nextflow pipeline which implements a genome browser session to visualize omics data. Then, it sets up an interactive genomes catalog based on the Keshif data visualization tool.

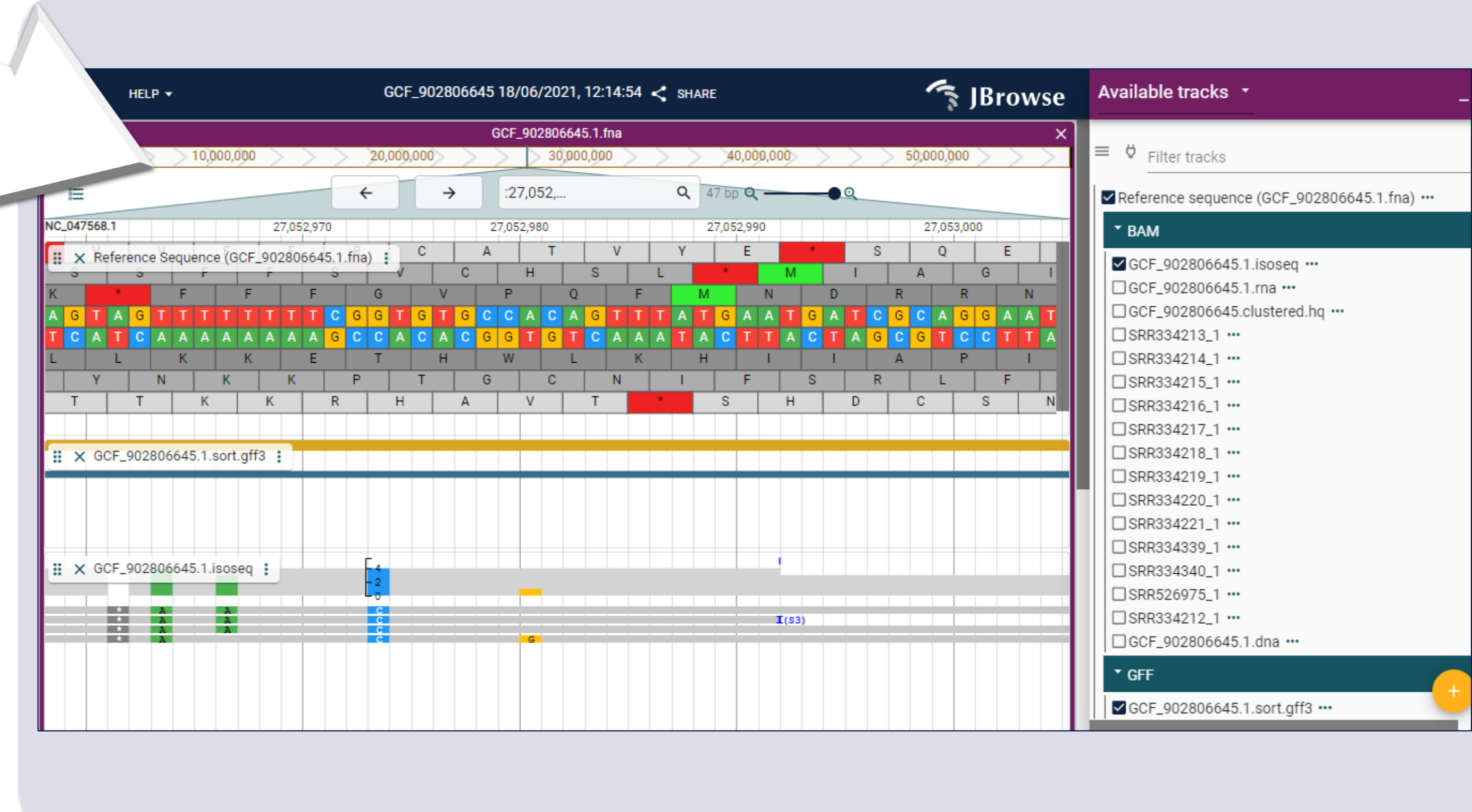
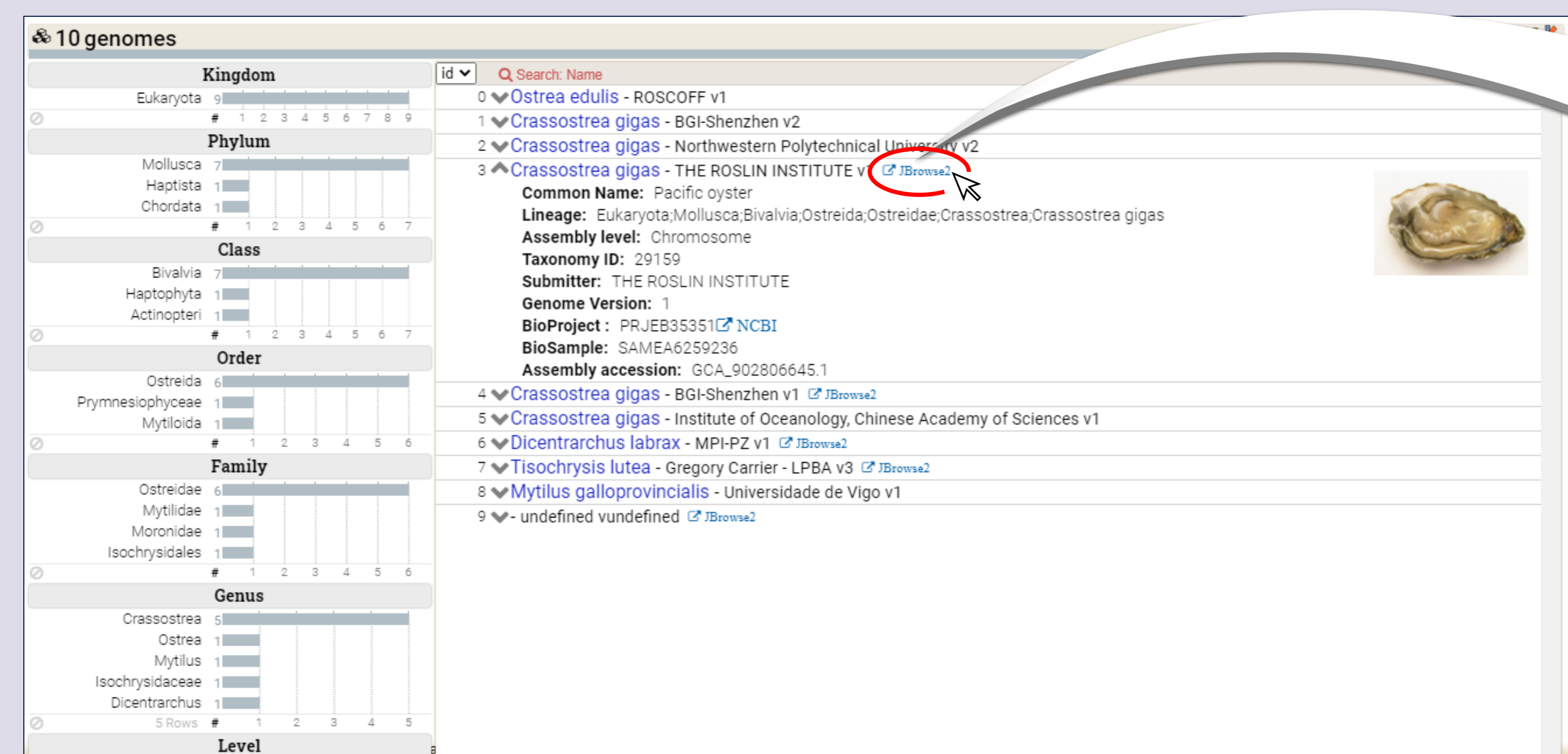
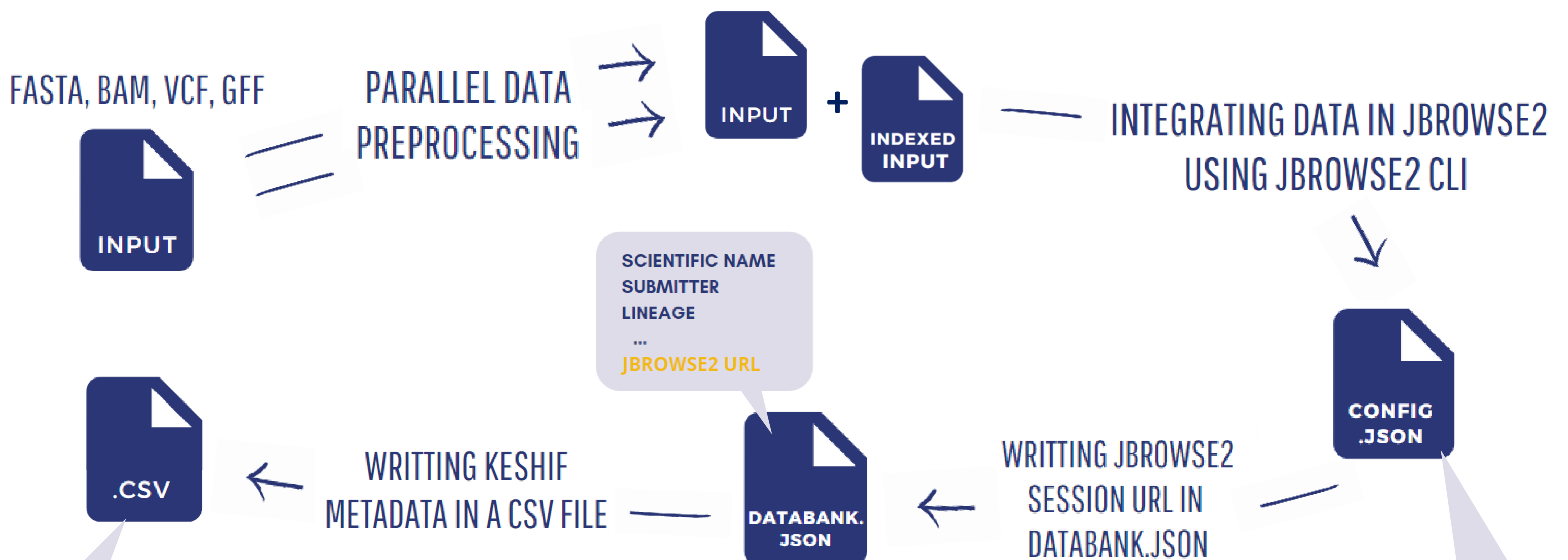
INTERACTIVE GENOME CATALOG

The catalog provides the list of available model organisms, along with metadata such as lineage, genome version, submitter, etc. The catalog enables view filtering through specific features defined according to the metadata.

GENOME BROWSER

To visualize omics data of model organisms, the catalog gives access to a genome browser session, implemented using JBrowse2 viewer. This tool provides fast and smooth scrolling and zooming.

OMICS-CATALOG PIPELINE



OMICS-CATALOG is freely available at :

<https://github.com/ifremer-bioinformatics/omics-catalog>

References :

- Adil Yalçın et al., 2016. *Proc. of IEEE VIS 2016 Workshop on Visualization in Practice*
- Buels et al., 2016. *Genome Biology*, 17: 66
- Di Tommaso et al., 2017 35(4):316-319